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<151> 1999-07-02

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                                      90
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Va	l Gl	n Cy	s Glı	ı Val	Gli	ı Let	ı Val	Glı	ı Sei	r Gly	Gly	y Asr	Lei	ı Va	l Ly:	S
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Ser	Ser	Туг	Gly	Met	Ser	Trp	Ile	Arg	Gln	Thr	Pro	Asp	Lys	Arg	Leu	!
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gag	tgg	gto	gca	acc	att	agt	agt	ggt	ggt	agt	tac	acc	tac	tat	cca	240
Glu	Trp	Val	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Tyr	Tyr	Pro	
				50					55					60		
gac	agt	gtg	aag	ggg	cga	ttc	acc	atc	tcc	aga	gac	aat	gcc	aag	aac	288
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
			65					70					75			
acc	cta	tac	ctg	caa	atg	agc	agt	ctg	aag	tct	gag	gac	aca	gcc	atg	336
Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	
		80					85					90				
ttt	tac	tgt	gca	aga	cag	act	ac t	atg	act	tac	ttt	gc t	tac	tgg	ggc	384
Phe	Tyr	Cys	Ala	Arg	Gln	Thr	Thr	Met	Thr	Tyr	Phe	Ala	Tyr	Trp	Gly	
	95					100					105					
caa	ggg	act	ctg	gtc	act	gtc	tct .	gca								411
Gln	Gly	Thr	Leu	Val '	Thr	Val :	Ser .	Ala								
110					115											
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75

336

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn

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70

65

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                                                    90
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                                                                      384
  Tyr Tyr Cys Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly
       95
                          100
                                               105
 cag gga acc ctg gtc acc gtc tcc tca
                                                                      411
 Gln Gly Thr Leu Val Thr Val Ser Ser
  110
                      115
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Ser Ala Ser Asn Arg Tyr Thr
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 Gln Gln His Tyr Ser Thr Pro Phe Thr
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                    5
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Pro Tyr Trp Met Gln
  1
                   5
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1

5

10

<210> 65

<211> 411

<212> DNA

<213> Mus musculus

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<222> (58).. (411)

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-15

-10

-5

tct ttc tcc caa ctt gtg ctc act cag tca tct tca gcc tct ttc tcc 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Ser Ser Ala Ser Phe Ser

-1 1

5

10

ctg gga gcc tca gca aaa ctc acg tgc acc ttg agt agt cag cac agt 144 Leu Gly Ala Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15

20

25

acg tac acc att gaa tgg tat cag caa cag cca ctc aag cct cct aag 192

<221> mat_peptide

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                        35
                                            40
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  tat gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg
                                                                      240
  Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
                   50
                                        55
                                                            60
  att eet gat ege tie tet gga tee age tet ggt get gat ege tae ett
                                                                     288
  lle Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu
               65
                                   70
                                                        75
  age att tee aac ate eag eea gaa gat gaa gea atg tae ate tgt ggt
                                                                     336
  Ser Ile Ser Asn Ile Gln Pro Glu Asp Glu Ala Met Tyr Ile Cys Gly
           80
                               85
                                                   90
 gtg ggt gat aca att aag gaa caa ttt gtg tat gtt ttc ggc ggt ggg
                                                                     384
 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
      95
                         100
                                              105
 acc aag gtc act gtc cta ggt cag ccc
                                                                    411
 Thr Lys Val Thr Val Leu Gly Gln Pro
 110
                     115
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411

acc aaa ctg acc gtc cta ggt cag ccc

Thr Lys Leu Thr Val Leu Gly Gln Pro

<210> 67

<211> 411

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<220>

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<222> (1).. (411)

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<222> (58).. (411)

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tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144 Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys
30 35 40 45

tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240

Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly 50 55 60 att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288 lle Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu 65 70 75 acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt 336 Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly 80 85 90 gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly 95 100 105 acc aaa ctg acc gtc cta ggc cag ccc 411 Thr Lys Leu Thr Val Leu Gly Gln Pro 110 115 <210> 68 <211> 411 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1).. (411) <220> <221> mat_peptide <222> (58).. (411)

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Me	t Al	a Tr	p Th	r Pr	o Le	u Pho	e Ph	e Ph	e Ph	e Va	l Le	u Hi	s Cy	's Se	r Gly	,
				-1	5				-10	0				-	5	
tc	t tt	c tc	c ca	g ct	t gt	g cts	g ac	t ca	a tc	g cc	c tc	t gc	c tc	t gc	c tcc	96
Se	r Ph	e Se	r Gli	n Lei	ı Va	l Lei	ı Thi	r Gla	n Sei	r Pro	o Se	r Ala	a Se	r Ala	a Ser	
		-	1	Ī			į	5				10)			
ct	g gg	a gc	c teg	ggto	aag	cto	aco	tgo	c acc	tte	g agi	agt	cas	g ca	c agt	144
Lei	ı Gly	y Ala	a Sei	Val	Lys	Leu	Thi	· Cys	s Thr	Leı	ı Sei	Ser	Glı	ı His	s Ser	
	15	5				20					25)				
ace	g tac	c acc	att	gaa	tgg	tat	cag	cag	g cag	cca	gag	aag	ggo	cct	aag	192
Thi	Tyr	Thi	· Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	Lys	Gly	Pro	Lys	
30)				35					40					45	
tac	gtg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
Tyr	Val	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
				50					55					60		
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
He	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu	
			65					70					75			
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	tac	tgt	ggt	336
Thr	He	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	
		80					85					90				
			aca													384
Val	Gly	Asp	Thr	He	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
	95					100					105					
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ccc								411
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln :	Pro								
110					115											

<210> 69

<211> 411

<212> DNA

<213> Homo sapiens

<220>

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<220>

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<222> (58).. (411)

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-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144 Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg 192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg

30 35 40 45

tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240 Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly

50 55 60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu 65 70 75 acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt 336 Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly 80

gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly 95 100 105

90

85

acc aaa ctg acc gtc cta ggc cag ccc 411 Thr Lys Leu Thr Val Leu Gly Gln Pro 110

115

<210> 70

<211> 411 <212> DNA

<213> Homo sapiens

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<222> (1).. (411)

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<222> (58).. (411)

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-15

-10

-5

tct	ttc	tcc	cag	ctt	gtg	ctg	act	caa	tcg	ссс	tct	gcc	tct	gcc	tcc	96
Ser	Phe	Ser	Gln	Leu	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ala	Ser	Ala	Ser	
		-1	1				5					10				
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Leu	Gly	Ala	Ser	Val	Lys	Leu	Thr	Cys	Thr	Leu	Ser	Ser	Gln	His	Ser	
	15					20					25					
acg	tac	acc	att	gaa	tgg	tat	cag	cag	cag	cca	gag	aag	ggc	cct	agg	192
Thr	Tyr	Thr	Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	Lys	Gly	Pro	Arg	
30					35					40					45	
tac	gtg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
Tyr	Val	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
				50					55					60		
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu	
			65					70					75			
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	tac	tgt	ggt	336
Thr	He	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	
		80					85					90				
gtg	ggt	gat	aca	att	aag	gaa	caa	ttt	gtg	tac	gtg	ttc	ggc	gga	ggg	384
Val	Gly	Asp	Thr	Ile	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
	95					100					105					
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ccc								411
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro								
110					115											

<210> 71

<211> 411

<212> DNA

<213≻ Homo sapiens

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acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt 336

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu

70

65

75

288

Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly 80 85 90 gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly 95 100 105 acc aaa ctg acc gtc cta ggc cag ccc 411 Thr Lys Leu Thr Val Leu Gly Gln Pro 110 115 <210> 72 <211> 411 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1).. (411) <220> <221> mat_peptide <222> (58).. (411) **<400>** 72 atg gcc tgg act cct ctc ttc ttc ttc ttt gtt ctt cat tgc tca ggt 48 Met Ala Trp Thr Pro Leu Phe Phe Phe Phe Val Leu His Cys Ser Gly -15-10-5 tet tte tee eag ett gtg etg act eaa teg eec tet gee tet gee tee 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser -1 1 5 10

ct	or or or	ാ സംഗ	e to	a at	e nn	r ot	0.00	a ta					,			
															c agt	
Lei	u GI	y Ala	a Se	r Va	l Lys	s Lei	u Thi	r Cys	s Th	r Lei	ı Sei	Sei	r Gla	n Hi	s Ser	
	15	5				20)				25)				
ace	g tao	c acc	ati	t gaa	a tgg	tai	cag	g cag	g cag	g cca	gag	aag	gg	c cc	t agg	192
Thr	Tyı	Thr	Ile	e Glu	ı Trp	Туг	Gln	Gln	Gln	Pro	Glu	Lys	Gly	7 Pro	Arg	
30)				35					40					45	
tac	ctg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
Tyr	Leu	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
				50					55					60)	
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
He	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu	
			65					70					75			
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	atc	tgt	ggt	336
Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Ile	Cys	Gly	
		80					85					90				
gtg	ggt	gat	aca	att	aag	gaa	caa	ttt	gtg	tac	gtg	ttc	ggc	gga	ggg	384
										Tyr						
	95					100					105					
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ссс								411
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro								
110					115											

<210> 73

<211> 411

<212> DNA

<213≻ Homo sapiens

<220>

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<222> (58).. (411)

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tet tte tee eag ett gtg etg act eaa teg eec tet gee tet gee tee 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser -1 5

10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144 Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser 15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192 Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys 30 35 40 45

tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240 Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly 50 55 60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288 Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu 65 70 75

acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt 336 Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly 80 85 90

gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly 95 100 105

acc aaa ctg acc gtc cta ggc cag ccc

411

Thr Lys Leu Thr Val Leu Gly Gln Pro

110

115

<210> 74

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<400> 74

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-15

-10

-5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96 Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1

5

10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144 Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15

20

25

acg	tac	acc	att	gaa	t gg	tat	cag	cag	cag	cca	gag	g aag	ggc	cct	agg	192
Thr	Tyr	Thr	Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	l Lys	Gly	Pro	Arg	
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t ac	gtg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
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Val	Gly	Asp	Thr	He	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
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